EXHIBIT B

Alignment of nucleotide sequences of glutamine synthetase genes

```
                    1                                              50
2247        (1)  -------------GTGGCGTTTGAA-ACCCCGGAAGAAATTGTCAAGTT
13032       (1)  -------------GTGGCGTTTGAA-ACCCCGGAAGAAATTGTCAAGTT
CEFgInA1    (1)  -------------GTGGCGTTTAAC-ACCCCGGAAGAAGTAACCAAGTT
CEFgInA2    (1)  ------GTGGCCTCGAGCCCGACAACCAACCCGGATGAGATCCTCAAGTT
MtugInA2    (1)  -------------------ATGGACCGACAGAAGGAATTCGTTCTTCG
MtugInA3    (1)  -----------------ATGACAGCCACACCGCTTGCCGCGGCCGCGAT
MtugInA4    (1)  GTGACCGGCCCCGGTTCGCCGCCGTTGGCGTGGACCGAGTTGGAGCGACT
MtugInA1    (1)  -------------GTGACGGAAAAG-ACGCCCGACGACGTCTTCAAACT
Consensus   (1)               GTGGCGGATGA  ACCCCGGA GAA T GTCAAGTT

                    51                                             100
2247       (36)  CATCA----AGGATGAA---AACGTCGAGTTCGTTGACGTTCGATTCACCG
13032      (36)  CATCA----AGGATGAA---AACGTCGAGTTCGTTGACGTTCGATTCACCG
CEFgInA1   (36)  CATCA----AGGATGAA---AACGTTGAGTTCGTCGATGTCCGATTCACCG
CEFgInA2   (45)  CATCC----GGGACAAT---GACATCAACTGGGTTGGACGTCCAGTTCACCG
MtugInA2   (30)  TACCC----TGGAAGAACGCGACATCCGCTTGGTCCGGCTGTGGTTCACAG
MtugInA3   (33)  CGCCCAATTGGAGGCAGAGGGCGTCGACACCGTCATCGGCACCGTCGTGA
MtugInA4   (51)  GGTCG----CGGCCGGT--GACGTCGACACCGTCATCGTCGCGTTCACCG
MtugInA1   (36)  TGCCA----AGGACGAG--AAGGTCGAATATGTCGACGTCCGGTTCTGTG
Consensus  (51)  CATCA    AGGA GAA    GACGTCGACTTCGTCGACGTCCGGTTCACCG

                    101                                            150
2247       (80)  ACCTTCCCGGCACCGAGCAGCACTTCAGCATCCCAGCTGCCAGCTTCGAT
13032      (80)  ACCTTCCCGGCACCGAGCAGCACTTCAGCATCCCAGCTGCCAGCTTCGAT
CEFgInA1   (80)  ACCTTCCCGGCAATCGAGCAGCACTTCAGCATCCCCGCATCCGCTCTTGAT
CEFgInA2   (89)  ACGTTCCCGGCACCGAACAGCACCTGTCCGTGCCCGCCGCGGCATTCGAC
MtugInA2   (77)  ACGTGCTCGGTTTTCCTCAAGTCGGTCGCCATCGCCCCAGCCGAACTCGA-
MtugInA3   (83)  ACCCCGCGCGGCACTCACCCAGGCCAAGACCGTGCCGATACGCCGGACCAA-
MtugInA4   (95)  ACATTGCAGGGC-------CGGCTGGCCGGCAAACGGATATCGGGGCCGGCA-
MtugInA1   (80)  ACCTGCCTGGCATCATGCAGCACTTCACGATTGCCGGCTTCGGCCGTTTGAC
Consensus (101)  ACCTTCCCGGCATCGAGCAGCACTTCAGCATCCCC GCAGCCGGCTTCGA

                    151                                            200
2247      (130)  GCAGATACAGTCGAAGAAGGTCTCGCATTCGACGGATCCTCGATCCGTGG
13032     (130)  GCAGATACAATCGAAGAAGGTCTCGCATTCGACGGATCCTCGATCCGTGG
CEFgInA1  (130)  GAGGACGCCATCGAGGAGGGCCTCGCCTTCGACGGTTCCTCCATCCGTGG
CEFgInA2  (139)  GAATCCGCCATGGAAAACGGACTGGCCTTCGAGGGGTCATCGATCAGCGG
MtugInA2  (126)  --GGGCGCCTTCGAGGAAGGCATCGCCTTCGACGGATCCTCGATCGAGGG
MtugInA3  (132)  ------CACATTCGCCAA--TCCTGGCCT-CGGCGGCCAGTCCGGTGTGGCA
MtugInA4  (138)  -------T--TTCGTCGACGACATAGCCACCGCGCGGCGTCGAGTGCTGCAG
MtugInA1  (130)  AAGAGCGGTGTTTGACGACGGCTTGGCCTTTGACGGCTCGTCGATTCGCGG
Consensus (151)  G  G CGC TTCGA GA GGCCTCGCCTTCGACGG TCCTCGATCCG GG

                    201                                            250
2247      (180)  CTTCACCACGATCGACGAATCTGACATGAATCTCCTGCCAGACCTC-GGA
13032     (180)  CTTCACCACGATCGACGAATCTGACATGAATCTCCTGCCAGACCTC-GGA
CEFgInA1  (180)  TTTCACCACCATTGATGAATCCGACATGAACCTGCTGCCGGATCTG-GCC
CEFgInA2  (189)  ATACACCACTGTCGACGATTCCGACATGATGCTGCTGCCGGATCTG-TCC
MtugInA2  (174)  CTTTGCGCGGGTCTCGGAATCCGATACGGTGGCGCACGCGGACC-------
MtugInA3  (174)  TACGTTCTGTATCGACCAATGCAGTATTGCATTCACCGCAGACATCAGTG
MtugInA4  (180)  TTATCTGCTGGCCGTGGACGTGGACCGTGAACACGGTGCCCGGCTAT-GCG
MtugInA1  (180)  GTTCCAGTCGGATCGCACGAATCCGACATGTTGCTTCTTCCCGATCCC-GAG
Consensus (201)  TTCACCACGATCGACGAATCCGACATGAA CTGCTGCC GACCTC G

                    251                                            300
```

1

```
2247      (229) ACGGCCACCCTTGATCC---ATTCCGCAA-----GGCAAAGACCCTGAACGT
13032     (229) ACGGCCACCCTTGATCC---ATTCCGCAA-----GGCAAAGACCCTGAACGT
CEFgInA1  (229) ACCGCGAAGATCGATCC---GTTCCGCAA-----GGCGAAGACCCTGAACAT
CEFgInA2  (238) ACGGCGTTCATCGACCC---GTTCCGCAG-----GTCGAAGACGCTCAACAT
MtugInA2  (218) -CGTCGACCTTCCAGGT---GCTGCCCTG-----GGCCA----CC-------
MtugInA3  (224) TGGTCGGCGATCAACGT----CTCCGCAT-----CGA----TC---------
MtugInA4  (229) ATGGCCAGTTGGGACACCGGCTACGGCGATATGCTGATGACGCCGGACTT
MtugInA1  (229) ACGGGCGCGCATCGACCC---GTTCCGCGC----GGCCAAGACGCTGAATAT
Consensus (251) ACGGCGACCATCGACCC   GTTCCGCA     GGCGAAGACCCTGAAC T
                 301                                              350
2247      (273) -TAAGTTCTTCGTTCACGATCCTTTCACCCGCGAGGCATTCTCCCGCGAC
13032     (273) -TAAGTTCTTCGTTCACGATCCTTTCACCCGCGAGGCATTCTCCCGCGAC
CEFgInA1  (273) -CAAGTTCTTCGTCCATGACCCCTTCACCCGTGAGGCGTTCTCCCGCGAC
CEFgInA2  (282) -CAAGTTCTTCGTCCATGACCCCTATACCCGGGAACCATTTTCCCGGGAT
MtugInA2  (250) ---AGTTC--CGGCCACCACCACT-CAGCGCGGATGTTTGCGAGATCA-
MtugInA3  (254) -T--GTCCGCCTTGCGCATCATCGGCGACGGCGTTGGCCGTG---GGCGGCCG
MtugInA4  (279) GTCCACTCTGCGGCTGATTCCTTGGCTACCGGGAACGGCGCTGGTGATCG
MtugInA1  (273) -CAACTTCTTTGTGCACGACCCGTTCACCCTGGAGCCGTACTCCCGCGAC
Consensus (301) TAAGTTCTTCGTCCACGACCCCTTCACCCGGGAGGCGTTCTCCCGCGAC
                 351                                              400
2247      (322) CGACGCAACGTAGCACGGCAAGGCAGAGCAGTACCTGGC----ATCCACCGG
13032     (322) CCACGCAACGTGGCACGGCAAGGCAGAGCAGTACCTGGC----ATCCACCGG
CEFgInA1  (322) CCCCGCAATGTGGCACGTAAGGCCGAGCAGTTCCTGGC----CTCCACCGG
CEFgInA2  (331) GCCCGCAACATCGCCCGCAAGGCGGAGGAGTACCTGGC----TTCCACCGG
MtugInA2  (293) CCATGCCGGACGGCTCGCC-GTCGTGGGCGGACCCG-----CGGCACGTG
MtugInA3  (299) GCGGGTTCTTCGAGCAGGACGGCACACCGGTCCCCGC----CTGCAGCCG
MtugInA4  (329) CCGACCTGGTCTGGGCCGACGGCAGCGAGGTCGCCGTCTCGCCGCGCGCAGC
MtugInA1  (322) CCGCCGCAACATCGCCCGCAAGGCCGAGAACTACCTGAT----CAGGCACTGG
Consensus (351) CC CGCAAC TGGC CGCAAGGCAGAGCAGTACCTGGC    CTGCACCGG
                 401                                              450
2247      (369) CATTGCAGACACCTGCAACTTCGGCGCCGAGGCTGAGTTCTACCTCTTCG
13032     (369) CATTGCAGACACCTGCAACTTCGGCGCCGAGGCTGAGTTCTACCTCTTCG
CEFgInA1  (369) GATCGCCGACACCTGCAACTTCGGCGCCGAGGCCGAGTTCTATCTCTTCG
CEFgInA2  (378) TTTCGCCGACAGCTGTAACTTCGGCGCCGAAGCCGAGTTCTACATCTTCG
MtugInA2  (337) TTGCGGCGGCAGCTG---ACGAAGGC--C--GGC-GAACTCGGCTTCTCCT
MtugInA3  (345) AGGAACACTGAGCCGGATCGAGGCCGCGCTTGCTGATGCCGGCATCGACG
MtugInA4  (379) ATTCTGCGCCGTCAGCTCGATCGGCT-CAAGGC----GCGCGGACTGGTCG
MtugInA1  (369) GATCGCCGACACCGCATACTTCGGCGCCGAGGCCGAGTTCTACATTTTCG
Consensus (401) CATCGCCGACACCTGCAACTTCGGCGCCGAGGC GAGTTCTACCTCTTCG
                 451                                              500
2247      (419) ACTCCGTTCGCTACTCCACCGAGATGAACTCCGGCTTCTACGAAGTAGAT
13032     (419) ACTCCGTTCGCTACTCCACCGAGATGAACTCCGGCTTCTACGAAGTAGAT
CEFgInA1  (419) ACTCCGTCGCGTTACTCCACCGACATCAACTCCGGTTTCTACCATGTGGAC
CEFgInA2  (428) ACTCCGTGCGGGTTCAGCTCCCAGTCCAATGCGGCATTCCACGAGGTGGAT
MtugInA2  (380) GCTACGTGCATCCCGAAATCGAG--------TTCTTCCTGCTCAAG
MtugInA3  (395) CGGTAATCGGCCACGAAGTCGAA----------TTCCTCTTGGTCGAC
MtugInA4  (425) CCGATGTGGCCACCGGAGCTGGAGTTCATCGT-G--TTCGACCAGCCGTAT
MtugInA1  (419) ATTCGGTGAGGCTTCGACTCGCGCGCCAACGGCTCCTTCTACGAGGTGGAC
Consensus (451) ACTCCGTGCGCTACGACACCGAG TCAAC CCG  TTCTACGAGGTGGAT
                 501                                              550
2247      (469) AGCGAAGAAGGCTGGTGGAACCGTGGCAAGGAAAACCAACCTCGACGGAAC
```

```
13032      (469) ACCGAAGAAGGCTGGTGGAACCGTGGCAAGGAAACCAACCTCGACGGCAC
CEFgInA1   (469) ACCAACGAGGGTTGGTGGAACCGTGGCCGTGAGACCAACCTCGATGGCAC
CEFgInA2   (478) TCCGTGGAGGGCTGGTGGAACAGTGGTTCCCGGGAGAACCCGGACGGCAG
MtugInA2   (418) CCC-----------GGACCGAGGACGGG-------TCCGTGCCCG
MtugInA3   (433) GCGGA-----C---G-GCCAGCGGCTGCCT-------TCGACG-CTG
MtugInA4   (472) CGCC---AGGCA---TGGGCCAGCGG----GTA--------TCGCGGGCTG
MtugInA1   (469) GCCATCTCGGGGTGGTGGAACACCGGCGCGGCGACCGAGGCCGACGGCAG
Consensus  (501) CCGA GAGGGCTGGTGGAACCGTGGC  GGA ACCAACCTCGACGGCAG
                 551                                              600
2247       (519) GCCAAACCTGGGCGCAAAGAACCGCGTCAAGGGCTGGCTACTTCCCAGTAG
13032      (519) GCCAAACCTGGGCGCAAAGAACCGCGTCAAGGGCTGGCTACTTCCCAGTAG
CEFgInA1   (519) CCCCAACACCGGTTCCAAGAACCGGCCTCAAGGGCGGTTACTTCCCCGTCG
CEFgInA2   (528) CAGGAACCTGGGTCACAAGGTACGCCAGAAGGGTTGGTTACTTCCCGGTGG
MtugInA2   (446) TCCC-----GGTCG--A-------CAACGCCGGCTATTTCGACCAAG
MtugInA3   (463) T-------GGGC------GC-------AGTACGG---TGTCGCGCGGGG
MtugInA4   (505) ACCC-----C-GGCC----AGCGA--CTACAACATCGACTACGCGATATTGG
MtugInA1   (519) TCCCAACCGGGGCTACAAGGTCCGCCCAAGGGCGGGGTATTTCCCAGTGG
Consensus  (551) CCCCAACC GGGCC  AAG  CCGC  CAAGGGCGGCTACTTCCCAGTGG
                 601                                              650
2247       (569) CA--CCATACGACCAAACCGTTGACGTGCGCGATGACATGGTTCGGCAACC
13032      (569) CA--CCATACGACCAAACCGTTGACGTGCGCGATGACATGGTTCGCAACC
CEFgInA1   (569) CA--CCCTACGACCAGACCGTGGACGTCCGCGATGAGATGGTCCGCAACC
CEFgInA2   (578) CA--CCCTATGACCACTTCCAGGACCTGCGCGACACCCATTGGTGAGACCC
MtugInA2   (479) CG--GTGCACGACTCCGCCTTGAACTTTCGCCGCCACGCGATCGATGCGCC
MtugInA3   (488) TG--CTCGAGCACGAGGCGTTCG----TCCGCGATGTCAACGCCGCGGCAA
MtugInA4   (545) CATCCTCGCGGATGGAGCCGGTTG--CTGCGCGACATCCGGTTGGGTA---
MtugInA1   (569) CC--CCCAACGACCGAATACGTCGACCTGCGCGGACAAGATGCTTGACCAACC
Consensus  (601) CA  CCCTACGACCAA CCGT GAC TGCGCGATGACATGGT GGCAACC
                 651                                              700
2247       (617) TCGCAGCTTCCGGCTTCGCTCTTGAGCGTTTCCACCACGAAGTCGG---T
13032      (617) TCGCAGCTTCCGGCTTCGCTCTTGAGCGTTTCCACCACGAAGTCGG---T
CEFgInA1   (617) TGCGTGACGCCGGTTTCCACCTGGAGCGTTTCCACCACGAGGTCGG---T
CEFgInA2   (626) TGGCGGAGATCGGGTTCACCGTGGAGCGTTCCCACCATGAGATGGGCAGT
MtugInA2   (527) TGGAATTCATGGGCATCTCGGTGGAGTTCAGCCATCACGAAGGCGC--A
MtugInA3   (533) CGGCAG----CAGGCATCGCTATCGAGCAGTTCCATCCCGAATACGG---T
MtugInA4   (590) TGGCCGGTGCGGGTCTTGCGATTCGAGGCGGTCAAAGGCGAATGCAA---C
MtugInA1   (617) TGATCAACTCCGGCTTCATCCTGGAGAAGGGCCACCGAGGTGGGCAGC
Consensus  (651) TGGCAG   CCGGCTTC C CTGGAGCGTTTCCACCACGAAGTCGG    T
                 701                                              750
2247       (664) GGCGGACAGCAGGAAATCAACTACCGCTTCAACACCATGCTCCACGCGGC
13032      (664) GGCGGACAGCAGGAAATCAACTACCGCTTCAACACCATGCTCCACGCGGC
CEFgInA1   (664) GGCGGCCAGCAGGAGATCAACTACCGCTTCAACACCGTCGTGCACGCAGC
CEFgInA2   (676) GGTGGTCAGCAGGAGATCAACTACCGTTTCAACACCGTGCTGCGCGCAGC
MtugInA2   (574) CCCGGCCAGCAGGAGATCGACCTGCCGGTTTGCCGACGCTCTGTCGATGGC
MtugInA3   (577) GCCAACCAATTCGAGATCTCGTTAGCGCCGCAGCCGGCCGGTCGCGGCCGC
MtugInA4   (637) ATGGGCCAGCAGGAGATCGGGTTTCGTTACGACGAGGCGCTGGTCACCTG
MtugInA1   (667) GGCGGACAGGCCGAGATCAACTACCAGTTCAATTCGCTGCTGCACGCCGC
Consensus  (701) GGCGGCCAGCAGGAGATCAACTACCG TTCAACACCCTGCTGCACGC GC
                 751                                              800
2247       (714) AGATGATATCCAGACCTTCAAGTACATCATCAAGAACACCGCTCGGCCTCC
13032      (714) AGATGATATCCAGACCTTCAAGTACATCATCAAGAACACCGCTCGGCGTCC
```

3

```
CEFglnA1   (714)  CGATGACATTCAGACCTTCAAGTACATCGTGAAGAACACCGCAGCCGTGC
CEFglnA2   (726)  CGATGACCTCCAGACCTTCAAGTACGTGGTGAAGAACACCGCGAAGGCCG
MtuglnA2   (624)  TGACAACGTGATGACCTTCCGCTACGTCATCAAAGAAGTCGCGGCTGGAAG
MtuglnA3   (627)  CGATCAGCTGGTGCTGACCCGCCTCATCATCGGCCGTACCGGCCGCCGGC
MtuglnA4   (687)  CGACAACCATGCGATCTACAAGAACGGCGCCAAGGAAATCGGCCGACCAGC
MtuglnA1   (717)  CGACGACATGCAGTTGTACAAGTACATCATCAAGAACACCGCCTGGCAGA
Consensus  (751)  CGATGACAT CAGACCTTCAAGTACATCATCAAGAACACCGC CGCC GC
                  801                                              850
2247       (764)  ACGGCAAGGCTGCAACCTTCATGCCCTAAGCCACTGGCTGGCGACAACGGT
13032      (764)  ACGGCAAGGCTGCAACCTTCATGCCCTAAGCCACTGGCTGGCGACAACGGT
CEFglnA1   (764)  ACGGCAAGGCTGCCACCTTCATGCCCAAGCCGCTGGCCGGTGACAACGGC
CEFglnA2   (776)  TCGGTAAATCCGCCACCTTCATGCCCAAGCCGCTGGCTGATGACGGCGGT
MtuglnA2   (674)  AGGGCGCCCGGGCGTCGTTCATGCCCAAGCCCATTCGGCCAGCACCCGGGC
MtuglnA3   (677)  ACGGGTTACGCGTGAGCCTATCGCCAGCGCCCTTCGCCGGAAGTATCGGA
MtuglnA4   (737)  ACGGCAAGAGCCTAACGTTCATGGCGAA---ATACGATGAACGCGAAGGT
MtuglnA1   (767)  ACGGGAAAACGGTCACGTTCATGCCCAAGCCGCTGTTCGCCGACAACGGCG
Consensus  (801)  ACGGCAAG C GC ACCTTCATGCCCAAGCCACTGGCTGG GACAACGGT
                  851                                              900
2247       (814)  TCCGGCATGCACGGCTCACCAGTCCCTCTGGAAGG----ACGGCAAGCCGACT
13032      (814)  TCCGGCATGCACGGCTCACCAGTCCCTCTGGAAGG----ACGGCAAGCCGACT
CEFglnA1   (814)  TCCGGCATGCACGGCCCACCAGTCCCTGTGGAAGG----ACGGCAAGCCGACT
CEFglnA2   (826)  TCCGGCATGCACATCCACCAGTCGCTGTGGAAGG----ACGGCAAGCCCCT
MtuglnA2   (724)  TCGGCGATGCACACCCACATGAGCCTGTTCGAGGGTGATGTCAACGCGGTT
MtuglnA3   (727)  TCCGGTGCCCACCAACACTTCTCGCTGACTATGTCGGAAGGGAT---GCT
MtuglnA4   (784)  AATAGCTGTCACATCCATGTCTCGCTGCGTGGCACGGATGGCTCCGCGGT
MtuglnA1   (817)  TCCGGCATGCACTGTCATCAGTCGCTGTGGAAGG----ACGGCGCCCCGCT
Consensus  (851)  TCCGGCATGCAC CCCACCAGTCGCTGTGGAAGG      ACGGCAAGCCGCT
                  901                                              950
2247       (861)  CTTCCACGATGA-GTCCGGGCTACGCAGGGCCTGTCCGAGATCGCCCGCGCTAC
13032      (861)  CTTCCACGATGA-GTCCGGGCTACGCAGGCCTGTCCGACATCGCCCGCTAC
CEFglnA1   (861)  CTTCCACGACGA-GTCCGGGCTACGCCGGCCTGTCCGACATCGCCCGTTAC
CEFglnA2   (873)  CTTCCATGATGA-GGCCGGTTATGCCAACCTGTCGGAGATGGCCCGTCAC
MtuglnA2   (774)  CCACAGCCGCTGATGATCCGCT--GCAG---CTGTCGGAAGTGGGTAAATCG
MtuglnA3   (774)  GTTCTCCGGTGG-GACTGGAGCAGCTGGCATGACCTCGGCCGGGGGAGGCC
MtuglnA4   (834)  GTTTGCCGACAGTAACGGGCCGCACGG-CATGTCGTCGATGTTCCGCCAGC
MtuglnA1   (864)  GATTGTACGACGA-GACGGCTTATGCCGGCTCTGTCGGACACGGCCCGTCAT
Consensus  (901)  CTTCCACGATGA GACCGGGCTACGC GGCCTGTCGGACATGGCCCG TAC
                  951                                              1000
2247       (910)  TACATCGGCCGGCATCCTGCACCACGCAGGCGCTGTTCTGGCCGTT-CACCA
13032      (910)  TACATCGGCCGGCATCCTGCACCACGCAGGCGCTGTTCTGGCCGTT-CACCA
CEFglnA1   (910)  TACATCGGTGGCATCCTCCACCACGCCGGTGCCGGTCCTGGCCGTT-CACCA
CEFglnA2   (922)  TATGTCGGTGGTCTGCTCAAGCATGCCCCCGCCGGGTGCTGGCTTTT-CACCA
MtuglnA2   (820)  TTCATCGCCCGGGATCCTGGAGCACGCTTGCGAGATCAGCGCGGGT-CACAA
MtuglnA3   (823)  GCGGTGGCAGGAGTGCTTC-GCGGACTACCGGACGCCCAAGGCATCCTGT
MtuglnA4   (883)  TTCGGTCGCCGGCCAGTTGG-CCACGTTGCGCGAATTCACGCTGTGCTATG
MtuglnA1   (913)  TACATCGGCCGGCCTGTTACACCACGCGCCGTGGCTGCTGGCCCTTT-CACCA
Consensus  (951)  TACATCGGCCGGCATGCTGCACCACGC GGCGCGGT CTGGCCGTT CACCA
                  1001                                             1050
2247       (959)  ACGGCAACCCTGAACTCCTACCACCGGTCTGGTTCCAGGGCTTCGAGGCTGCA
13032      (959)  ACGGCAACCCTGAACTCCTACCACCGGTCTGGTTCCAGGGCTTCGAGGCTCCA
CEFglnA1   (959)  ACCCGACGCCTGAACTCCTACCATCGCCTGGTGCCCGGGCTTCGAGGCGCCC
```

4

```
CEFgInA2   (971)  ACCCGACCCTGAATTCCTACAACCGTCTGGTGCCCGGTTTCGAGGCCCCG
MtugInA2   (869)  ATCAGTGGGTCAACTCTTACAAGCGGCTGGTGCAGGGCGGCGAAGCGCCC
MtugInA3   (872)  GCGGATCGATCGTGTCCGGTCTGCGAATGCGACCCGGTAACTGGGCCGGA
MtugInA4   (932)  CGCCGACCATTAACTCCTACAAGCGATTTGCCGATAGCAGTTTCGCGCCG
MtugInA1   (962)  ACCCGACGGTGAACTCCTACAAGCGGCTGGTTCCCGGTTACGAGGCCCCG
Consensus (1001)  ACCCGACCCTGAACTCCTACCAGCG CTGGT CC GGCTTCGAGGCCCC
                  1051                                            1100
2247       (1009) ATCAACCTGGTGTACTCACAGCGGCAACCGTTCCGCTGCTGTCCGTATCCC
13032      (1009) ATCAACCTGGTGTACTCACAGCGGCAACCGTTCCGCTGCTGTCCGTATCCC
CEFgInA1   (1009) ATCAACCTGGTCTACTCCCAGCGCAACCGCTCCGCGGCCGTGCCGTATCCC
CEFgInA2   (1021) GTGAGCCTGGCGTATTCGCGAGCAGAACCGTTCCGCCGCGATCCGCATTCC
MtugInA2   (919) ACGGCCGCGTCGTGGGGGGCCGCCAACCGATCCGCCCTAGTGCGGGTGCC
MtugInA3   (922) ATCTATGCATGCTGGGGTACCGAAAACCGGGAAGCGGCGGTGCCGATTCGT
MtugInA4   (982) ACGGCGCTGGCTTGGGGGGCTGGACAATCGCACCTGCGCCCTGCCGGGTG--
MtugInA1   (1012) ATCAACCTGGTCTATAGCCAGCGCAACCGGTCGGGCATGCGTGCGCATCCC
Consensus (1051) ATCAACCTGGTGTA TG CAGCGCAACCG TCCGC GC GTGCG ATCCC
                  1101                                            1150
2247       (1059) AAT---CACCGGATCCAACCCAAAGGCAAAGCGCATCGAATTCCGCGCTC
13032      (1059) AAT---CACCGGATCCAACCCGAAGGCAAAGCGCATCGAATTCCGCGCTC
CEFgInA1   (1059) GAT---CACCGGTTCCAACCCGAAGGCCAAGCGGCATCGAGTTCCGCGCAC
CEFgInA2   (1071) GGC---CAGCGGTCCCAACCCGAAGGCGACCCGCATCGAGTTCCGCACCC
MtugInA2   (969) GATGTACACGGCCGCACAAGACCTCGTCGCGGCGCGGTCGAAGTACGCAGGC
MtugInA3   (972) CAAGGGCGGGGCTGGCAGCGCGTACGGCGCGAACGTGGAGCGTGAAGGTCG
MtugInA4   (1030) GTTGGCCACGGG---CAAAACAT---C---CGGGTCGAATGCCGGGTTC
MtugInA1   (1062) GAT---CACCGGCAGCAACCCGGAAGGCCAAGCGGCTGGAGTTCCGAAGGC
Consensus (1101) GAT    CACCGG  CCAACCCGAAGGC AAGCGCATCGAGTTCCGCGCCC
                  1151                                            1200
2247       (1106) CAGACCCATCAGGCAACCCATACCTGGGCTTCGGCAGCGATGATGATGGCC
13032      (1106) CAGACCCATCAGGCAACCCATACCTGGGCTTTGGCAGCGATGATGATGGCC
CEFgInA1   (1106) CGGACCCATCCGGCAACCCCTACCTGGGCTTCGGCGGCATGATGATGGCC
CEFgInA2   (1118) CGGACCCCTCGGGTAACCCCTACCTGGCCGTTCACCGCGTCGATGATGGCG
MtugInA2   (1019) CTGATTCGGCGTGCAATCCCTATCTGACATTCGCCCGTGCTGCTGGCCGCG
MtugInA3   (1022) TCGACCCGTCGGCCAACCCGTATCTCGCGTCGGCGGCGGATCCTCGGACTG
MtugInA4   (1070) GCCGCGGTGATGTCAACCAGTACCTGGCCGGTGGCGGGCTCTTCATTGCTGGA
MtugInA1   (1109) CCGACTCGTCGGGCAACCCGTATCTGGCCGTTCTCGGCCATGCTGATGGCA
Consensus (1151) C GACCC TCGGGCAACCC TACCTGGCGTTCGC GCGATGATGATGGC
                  1201                                            1250
2247       (1156) GGCCTCGACGGCATCAAGAACCGGCATCGAGCCACACGCTCCAGTGGACAA
13032      (1156) GGCCTCGACGGCATCAAGAACCGGCATCGAGCCACACGCTCCAGTGGACAA
CEFgInA1   (1156) GGCCTGGACGGTGTGAAGAACCGGCATCGAGCCGCACGCACCGGTGGACAA
CEFgInA2   (1168) GGCCTGGACGGCATCCGCAACCGCATCGAACCCGACGCCCTCTGGACAA
MtugInA2   (1069) GGATTGCGGGGTGTAGAGAAGGGTTACGTGCTGGGCCCGCAGGCCGAGGA
MtugInA3   (1072) GCACTCGACGGCATGAAGACCAAGGCGGTGTTGCCGTCGGGAAACGACGGT
MtugInA4   (1120) GGGTTGTACGGTATCGAGCGGCGGCCTTTCAGCTGCCCGAGCCTGTGTCGG
MtugInA1   (1159) GGCCTGGACGGTATCAAGAACAAGATCGAGCCGCAGGCGCGCCGTCGACAA
Consensus (1201) GGCCTGGACGGTATCAAGAACCGCATCGAGCCGCACGCGCC GTGGACAA
                  1251                                            1300
2247       (1206) GGACCTCTACGAACTGCCACCAGAGGAAGCTGCATCCAT-------TCCAC
13032      (1206) GGACCTCTACGAACTACCACCAGAGGAAGCTGCATCCAT-------TCCAC
CEFgInA1   (1206) GGACCTCTACGAGCTCCCACCGGAGGAGGCCGCCTCCAT-------GCCGC
CEFgInA2   (1218) GGACCTCTATGAGCTCCCCGCCGAGGAGGCTGCCAAGGT-------CGCCG
```

5

```
MtuglnA2   (1119) CAACGTATGGGGACCTCACACCCGAGGAACGCCGAGCGATGGGGTACCGAG
MtuglnA3   (1122) AGACCCGACACAGCTGTCTGACGTGGATCGTGACCGTGCCGGCATTCTGC
MtuglnA4   (1170) CAACG-------CCT---ACC-----AAGGCGCCGATGT------CGAAC
MtuglnA1   (1209) GGATCTCTACGAGCTGCCGCCGGAAGAGGCCGCGAGTAT------CCCGC
Consensus  (1251) GGACCTCTACGAGCT CCACC GAGGAAGCTGCC C AT     CCCAC
                  1301                                            1350
      2247 (1250) AGGCACCAACCTCCCTGGAAGCATCCCTGAAGGCACTGCAGGAAGACACC
     13032 (1250) AGGCACCAACCTCCCTGGAAGCATCCCTGAAGGCACTGCAGGAAGACACC
  CEFglnA1 (1250) AGGCACCGACCTCCCTGGAGGCATCCCTGAAGGCCCTGCAGGAGGACTCC
  CEFglnA2 (1262) AGGCCCCACCTCACTGGAACAGGCGCTGAAGGCCCTGGAGGAGGACCAC
   MtuglnA2 (1169) AATTGCCGTCCAGTTTGGATAGTGCGCTGCGCGCCATGGAGGC---CTCC
   MtuglnA3 (1172) GACTTGCTGCCGATCAGGCGGATGCAATTGCTGTACTGGATAG----TTC
   MtuglnA4 (1199) GGCTGCCGGTTACGCTGGCCGACGCCGCGGTGCTGTTCGAGGA---TTCT
   MtuglnA1 (1253) AGACTCCGACCCAGCTGTCAGATGTGATCGACCGTCTCGAGGCCGACCAC
  Consensus (1301) AGGC CCGACCTC CTGGAAGA GCCCTGAAGGC CTGGAGGA GACTCC
                  1351                                            1400
      2247 (1300) GACTTCCTCACCGAGTCTGACGTCTTCACCGAGGATCTCATCGA-GGCGT
     13032 (1300) GACTTCCTCACCGAGTCTGACGTCTTCACCGAGGATCTCATCGA-GGCGT
  CEFglnA1 (1300) GACTTCCTCACCGAGTCCGACGTGTTCACCGAGGACCTCATCGA-GGCCT
  CEFglnA2 (1312) GAGTTCCTCACCGAGGGTGACGTGTTCACCGATGATCTCATCGA-GGCCT
   MtuglnA2 (1216) GAACTCGTCGCGGAG------GCCTTGGGGGAGCACGTTTTTGA-CTTTT
   MtuglnA3 (1218) GAAACTGCTTCGGTG------CATCCTTGGCGATCCCGTGGTAGATGCCGT
   MtuglnA4 (1246) GCGCTGGTGCGCGAG------GCGTTCGGCGAGGATGTTGTCGC-GCACT
   MtuglnA1 (1303) GAATACCTCACCGAAGGAGGGGTGTTCACAAACGACCTGATCGA-GACGT
  Consensus (1351) GA TTCCTCACCGAG    GACGTGTTCACCGAGGATCTCATCGA GGCGT
                  1401                                            1450
      2247 (1349) ACATCCAGTACAAGTAC---GACAACGAGATCTCCCCAGTTCGGCCTGCGC
     13032 (1349) ACATCCAGTACAAGTAC---GACAACGAGATCTCCCCAGTTCGCCCTGCGC
  CEFglnA1 (1349) ACATCCAGTACAAGTAC---GACAACGAGATCACCCCGGTCGGCCTGCGC
  CEFglnA2 (1361) ATGTGGCCTACAAGCAT---GAACATGAGATCACCCCTGAGCGCTCTGCGC
   MtuglnA2 (1259) TCTTGCGCAACAAGCGCACGGAGTGGGCGAACTACCGCAGCCACGTCACG
   MtuglnA3 (1263) GGTCGCGGTACGCCAGT-TAGAGCATGAGCGCTAC---GGTGACCTCGAT
   MtuglnA4 (1289) ACCTGAACAACGCGCCGTGTGGAGCTGGCGGCGTTCAACCGCGGCGGTCA---
   MtuglnA1 (1352) GGATCAGTTTCAAGCGC---GAAAACGAGATCGAGCCGGTCAACCATCCCG
  Consensus (1401) ACATGCAGTACAAGCGC   GA AACGAGATCTCCCC GT CGCCTGCGC
                  1451                                         1495
      2247 (1396) CCAAGCCCGCAGGAATTCGAATTGTACTTCGACTGC----------
     13032 (1396) CCAACCCCGCAGGAATTCGAATTGTACTTCGACTGCTAA-------
  CEFglnA1 (1396) CCCACCCCGCAGGAGTTCGAGCTGTACTTCGACTGCTAG-------
  CEFglnA2 (1408) CCCACCGCTCTGGATTTCGAGCTGTACTACGACTGCTAG-------
   MtuglnA2 (1309) CCATACGAGCTGCGCACGTACCTGTCGCTGTAG-------------
   MtuglnA3 (1309) GCTGCGCAGCTGGCCGACAAGTTCCGGATGGCTTGGAGTGTGTAA
   MtuglnA4 (1337) CCGATTGGGAGAGGATACGTGGATTTGAGCGCCTCTAG-------
   MtuglnA1 (1399) CCGCATCCCTACGAATTCGCGCTGTACTACGACGTTTAA-------
  Consensus (1451) CC ACCCCGCAGGAATTCGAGCTGTACTTCGACTGCTA
```

2247 : B.flavum ATCC14067
13032: C.glutamicum ATCC13032
CEF: C.efficiens YS314
Mtu: Mycobacterium tuberculosis H37RV

6